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IN RE PATENT APPLICATION OF

HARBERD et al

Atty. Ref.: 620-157

Serial No.: 09/911,513

Group Art Unit: 1638

Filed: July 25, 2001

Examiner: Mehta, A.

For: NUCLEIC ACID ENCODING GAI GENE OF ARABIDOPSIS THALIANA

* * * * *

December 19, 2002

SUBMISSION OF FORMAL DRAWINGS

Hon. Commissioner of Patents
and Trademarks
Washington, DC 20231

Attn: Official Draftsperson

Sir:

Enclosed herewith are 13 sheets of formal, inked
drawings for the above-identified application.

Respectfully submitted,

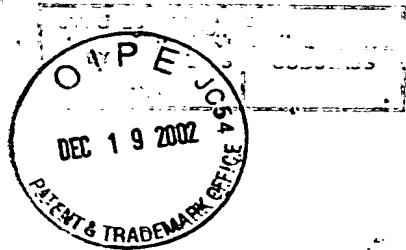
NIXON & VANDERHYE, P.C.

By Mary J. Wilson
Mary J. Wilson
Reg. No. 32,955

MJW:tat

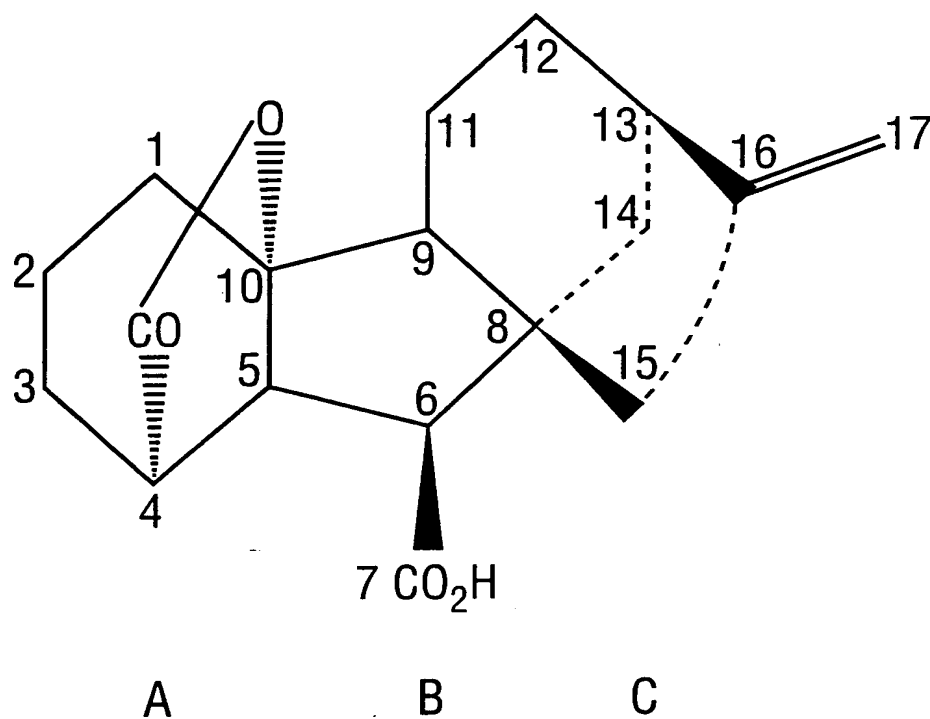
1100 North Glebe Road
8th Floor
Arlington, Virginia 22201-4714
Telephone: (703) 816-4000
Facsimile: (703) 816-4100

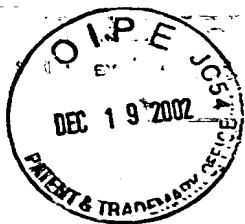
10
Formal
Drawings



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FIG. 1





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FIG. 2a



FIG. 2b

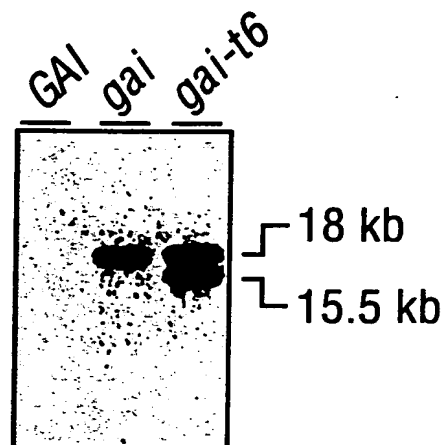
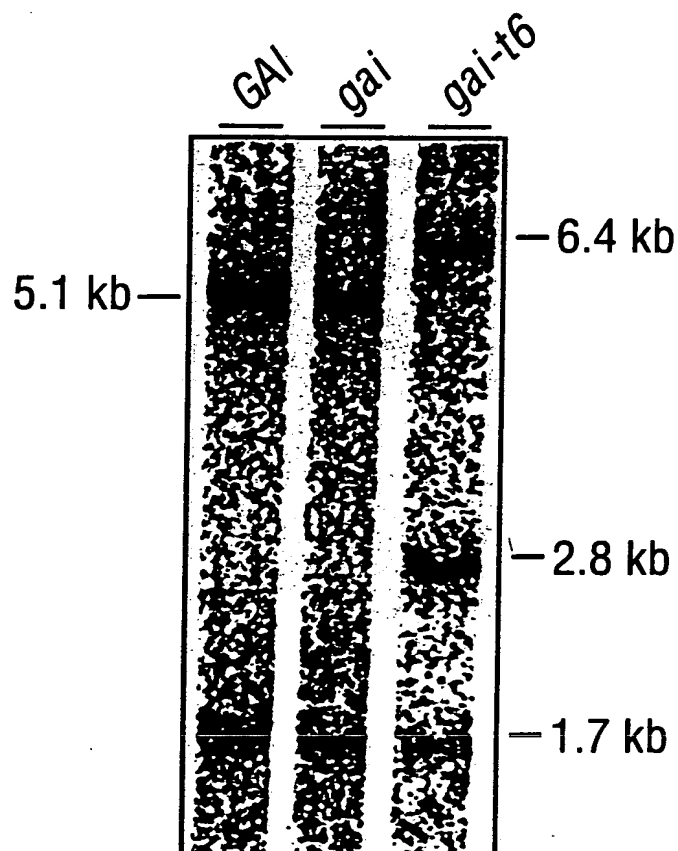


FIG. 2c





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Figure 3

TAATAATCAT	TTTTTTTCTT	ATAACCTTCC	TCTCTATTTT	TACAATTTAT	TTTGTATTAA	60
GAAGTGGTAG	TGGAGTGAAA	AAACAAATCC	TAAGCAGTCC	TAACCGATCC	CCGAAGCTAA	120
AGATTCTTCA	CCTTCCCAA	TAAAGCAAAA	CCTAGATCCG	ACATTGAAGG	AAAAACCTTT	180
TAGATCCATC	TCTGAAAAA	AACCAACCAT	GAAGAGAGAT	CATCATCATC	ATCATCAAGA	240
TAAGAAGACT	ATGATGATGA	ATGAAGAAGA	CGACGGTAAC	GGCATGGATG	AGCTTCTAGC	300
TGTTCTTGGT	TACAAGGTTA	GGTCATCGGA	AATGGCTGAT	GTTGCTCAGA	AACTCGAGCA	360
GCTTGAAGTT	ATGATGTCTA	ATGTTCAAGA	AGACGATCTT	TCTCAACTCG	CTACTGAGAC	420
TGTTCACTAT	AATCCGGCGG	AGCTTTACAC	GTGGCTTGAT	TCTATGCTCA	CCGACCTTAA	480
TCCTCCGTCG	TCTAACGCCG	AGTACGATCT	TAAAGCTATT	CCCGGTGACG	CGATTCTCAA	540
TCAGTTCGCT	ATCGATTCGG	CTTCTTCGTC	TAACCAAGGC	GGCGGAGGAG	ATACGTATAC	600
TACAAACAAG	CGGTTGAAAT	GCTCAAACGG	CGTCGTGGAA	ACCACCACAG	CGACGGCTGA	660
GTCAACTCGG	CATGTTGTCC	TGGTTGACTC	GCAGGAGAAC	GGTGTGCGTC	TCGTTACCGC	720
GCTTTTGGCT	TGCGCTGAAG	CTGTTCAGAA	GGAGAATCTG	ACTGTGGCGG	AAGCTCTGGT	780
GAAGCAAATC	GGATTCTTAG	CTGTTTCTCA	AATCGGAGCT	ATGAGAAAAG	TCGCTACTTA	840
CTTCGCCGAA	GCTCTCGCGC	GGCGGATTTA	CCGTCTCTCT	CCGTGCGAGA	GTCCAATCGA	900
CCACTCTCTC	TCCGATACTC	TTCAGATGCA	CTTCTACGAG	ACTTGTCTTT	ATCTCAAGTT	960
CGCTCACTTC	ACGGCGAATC	AAGCGATTCT	CGAAGCTTTT	CAAGGGAAGA	AAAGAGTTCA	1020
TGTCATTGAT	TTCTCTATGA	GTCAAGGTCT	TCAATGGCCG	GCGCTTATGC	AGGCTCTTGC	1080
GCTTCGACCT	GGTGGTCCTC	CTGTTTTCCG	GTTAACCGBA	ATTGGTCCAC	CGGCACCGGA	1140
TAATTTTCGAT	TATCTTCATG	AAGTTGGGTG	TAAGCTGGCT	CATTTAGCTG	AGGCGATTCA	1200
CGTTGAGTTT	GAGTACAGAG	GATTTGTGGC	TAACACTTTA	GCTGATCTTG	ATGCTTCGAT	1260
GCTTGAGCTT	AGACCAAGTG	AGATTGAATC	TGTTGCGGTT	AACTCTGTTT	TCGAGCTTCA	1320
CAAGCTCTTG	GGACGACCTG	GTGCGATCGA	TAAGGTTCTT	GGTGTGGTGA	ATCAGATTAA	1380
ACCGGAGATT	TTCACTGTGG	TTGAGCAGGA	ATCGAACCAT	AATAGTCCGA	TTTTCTTAGA	1440
TCGGTTTACT	GAGTCGTTGC	ATTATTACTC	GACGTTGTTT	GACTCGTTGG	AAGGTGTACC	1500
GAGTGGTCAA	GACAAGGTCA	TGTCGGAGGT	TTACTTGGGT	AAACAGATCT	GCAACGTTGT	1560
GGCTTGTGAT	GGACCTGACC	GAGTTGAGCG	TCATGAAACG	TTGAGTCAGT	GGAGGAACCG	1620
GTTCCGGTCT	GCTGGGTTTG	CGGCTGCACA	TATTGGTTCC	AATGCGTTTA	AGCAAGCGAG	1680
TATGCTTTTG	GCTCTGTTCA	ACGGCGGTGA	GGGTATCCG	GTGGAGGAGA	GTGACGGCTG	1740
TCTCATGTTG	GGTTGGCACA	CACGACCGCT	CATAGCCACC	TCGGCTTGG	AACTCTCCAC	1800
CAATTAGATG	GTGGCTCAAT	GAATTGATCT	GTTGAACCGG	TTATGATGAT	AGATTTCCGA	1860
CCGAAGCCAA	ACTAAATCCT	ACTGTTTTTC	CCTTTGTCAC	TTGTAAAGAT	CTTATCTTTC	1920
ATTATATTAG	GTAATTGAAA	AATTTCTAAA	TTACTCACAC	TGGC		1964

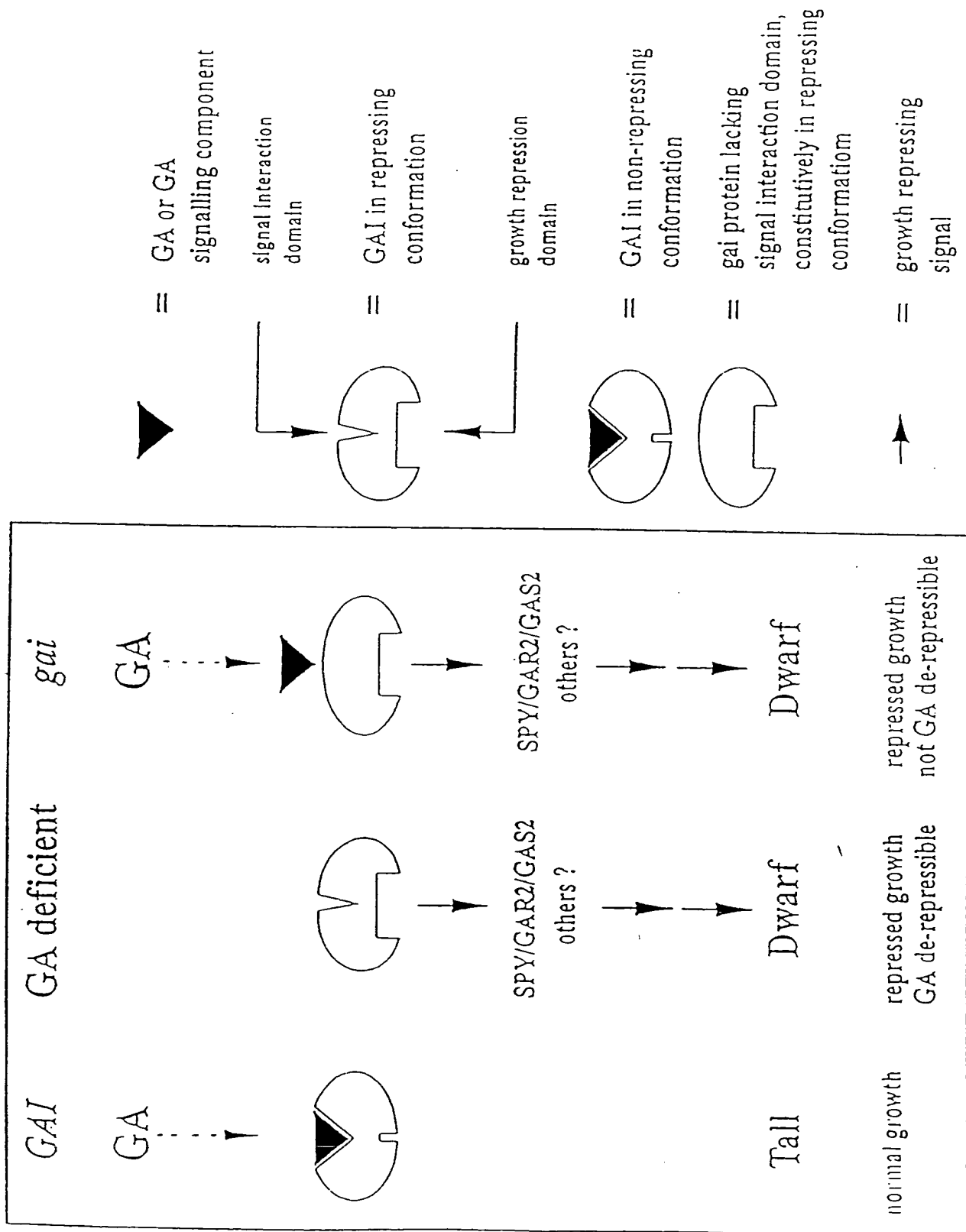


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Figure 4

MetLysArgAspHisHisHisHisHisGlnAspLysLysThrMetMetMetAsnGluGlu	20
AspAspGlyAsnGlyMet <u>AspGluLeuLeuAlaValLeuGlyTyrLysValArgSerSer</u>	40
<u>GluMetAla</u> AspValAlaGlnLysLeuGluGlnLeuGluValMetMetSerAsnValGln	60
GluAspAspLeuSerGlnLeuAlaThrGluThrValHisTyrAsnProAlaGluLeuTyr	80
ThrTrpLeuAspSerMetLeuThrAspLeuAsnProProSerSerAsnAlaGluTyrAsp	100
LeuLysAlaIleProGlyAspAlaIleLeuAsnGlnPheAlaIleAspSerAlaSerSer	120
SerAsnGlnGlyGlyGlyGlyAspThrTyrThrThrAsnLysArgLeuLysCysSerAsn	140
GlyValValGluThrThrThrAlaThrAlaGluSerThrArgHisValValLeuValAsp	160
SerGlnGluAsnGlyValArgLeuValHisAlaLeuLeuAlaCysAlaGluAlaValGln	180
LysGluAsnLeuThrValAlaGluAlaLeuValLysGlnIleGlyPheLeuAlaValSer	200
GlnIleGlyAlaMetArgLysValAlaThrTyrPheAlaGluAlaLeuAlaArgArgIle	220
TyrArgLeuSerProSerGlnSerProIleAspHisSerLeuSerAspThrLeuGlnMet	240
HisPheTyrGluThrCysProTyrLeuLysPheAlaHisPheThrAlaAsnGlnAlaIle	260
LeuGluAlaPheGlnGlyLysLysArgValHisValIleAspPheSerMetSerGlnGly	280
LeuGlnTrpProAlaLeuMetGlnAlaLeuAlaLeuArgProGlyGlyProProValPhe	300
ArgLeuThrGlyIleGlyProProAlaProAspAsnPheAspTyrLeuHisGluValGly	320
CysLysLeuAlaHisLeuAlaGluAlaIleHisValGluPheGluTyrArgGlyPheVal	340
AlaAsnThrLeuAlaAspLeuAspAlaSerMetLeuGluLeuArgProSerGluIleGlu	360
SerValAlaValAsnSerValPheGluLeuHisLysLeuLeuGlyArgProGlyAlaIle	380
AspLysValLeuGlyValValAsnGlnIleLysProGluIlePheThrValValGluGln	400
GluSerAsnHisAsnSerProIlePheLeuAspArgPheThrGluSerLeuHisTyrTyr	420
SerThrLeuPheAspSerLeuGluGlyValProSerGlyGlnAspLysValMetSerGlu	440
ValTyrLeuGlyLysGlnIleCysAsnValValAlaCysAspGlyProAspArgValGlu	460
ArgHisGluThrLeuSerGlnTrpArgAsnArgPheGlySerAlaGlyPheAlaAlaAla	480
HisIleGlySerAsnAlaPheLysGlnAlaSerMetLeuLeuAlaLeuPheAsnGlyGly	500
GluGlyTyrArgValGluGluSerAspGlyCysLeuMetLeuGlyTrpHisThrArgPro	520
LeuIleAlaThrSerAlaTrpLysLeuSerThrAsn	532

Figure 5





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Figure 6(a)

1 TAGAAGTGGT AGTCGAGTGA AAAAAACAAAT CCTAAGCAGT CCTAACCGAT
51 CCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTGTGCTCAG AAACCTCGAGC
251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA
351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
401 TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTCGC TATCGATTCTG
451 GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA
501 GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
551 AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CGGTGTGCGT
601 CTCGTTACAG CGCTTTTGGC TTGCGCTGAA GCTGTTTCTG AGGAGAATCT
651 GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTTCTC
701 AAATCGGAGC TATGAGAAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
751 CGGCGGATTT ACCGTCTCTC TCCGTGCGAG AGTCCAATCG ACCACTCTCT
801 CTCCGATACT CTTTAGATGC ACTTCTACGA GACTTGTCCT TATCTCAAGT
851 TCGCTCACTT CACGGCGAAT CAAGCGATTC TCGAAGCTTT TCAAGGGAAG
901 AAAAGAGTTC ATGTCATTGA TTTCTCTATG AGTCAAGGTC TTCAATGGCC
951 GGCGCTTATG CAGGCTCTTG CGCTTCGACC TGGTGGTCTT CCTGTTTCTC
1001 GGTAAACCGG AATTGGTCCA CCGGCACCGG ATAATTTCTGA TTATCTTCAT
1051 GAAGTTGGGT GTAAGCTGGC TCATTTAGCT GAGGCGATTC ACGTTGAGTT
1101 TGAGTACAGA GGATTTGTGG CTAACACTTT AGCTGATCTT GATGCTTCGA
1151 TGCTTGAGCT TAGACCAAGT GAGATTGAAT CTGTTGCGGT TAACTCTGTT
1201 TTCGAGCTTC ACAAGCTCTT GGGACGACCT GGTGCGATCG ATAAGGTTCT
1251 TGGTGTGGTG AATCAGATTA AACC GGAGAT TTTCACTCTG GTTGAGCAGG
1301 AATCGAACCA TAATAGTCCG ATTTTCTTAG ATCGGTTTAC TGAGTCGTTG
1351 CATTATTACT CGACGTGTGT TGAATCGTTG GAAGGTGTAC CGAGTGGTCA
1401 AGACAAGGTC ATGTCGGAGG TTTACTTGGG TAAACAGATC TGCAACGTTG
1451 TGGCTTGTGA TGGACCTGAC CGAGTTGAGC GTCATGAAAC GTTGAGTCAG
1501 TGGAGGAACC GGTTCGGGTC TGCTGGGTTT GCGGCTGCAC ATATTGCTTC
1551 GAATGCGTTT AAGCAAGCGA GTATGCTTTT GGCTCTGTTC AACGGCGGTG
1601 AGGGTTATCG GCTGGAGGAG AGTGACGGCT GTCTCATGTT GCG



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Figure 6(b)

1 MKRDHHHHHQ DKKTMMNNEE DDGNMGMDVAQ KLEQLEVMMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTTNKRLK CSNGVVETTT ATAESTRHVV LVDSQENGVR
151 LVHALLACAE AVQKENLTVA EALVKQIGFL AVSQIGAMRK VATYFAEALA
201 RRIYRLSPSQ SPIDHSLSDT L*



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Figure 6(c)

1 TAGAAGTGGT AGTGGAGTGA AAAACAAAT CCTAAGCAGT CCTAACCGAT
51 CCCC GAAGCT AAAGATTCTT CACCTTCCCA AATAAGCAA AACCTAGATC
101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTGCTCAG AAACCTCGAGC
251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA
351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
401 TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTCGC TATCGATTCTG
451 GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA
501 GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
551 AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CCGTGTGCGT
601 CTCGTTACAG CGCTTTTGGC TTGCGCTGAA GCTGTTTACA AGGAGAATCT
651 GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTTCTC
701 AAATCGGAGC TATGAGAAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
751 CGGCGGATTT ACCGTCTCTC TCCGTGCGAG AGTCCAATCG ACCACTCTCT
801 CTCCGATACT CTTCAGATGC ACTTCTACGA GACTTGTCCT TATCTCAAGT
851 TCGCTCACTT CACGGCGAAT CAAGCGATTC TCGAAGCTTT TCAAGGGAAG
901 AAAAGAGTTC ATGTCATTGA TTCTCTATGA GTCAAGGTCT TCAATGGCCG
951 GCGCTTATGC AGGCTCTTGC ECTTCGACCT GGTGGTCCTC CTGTTTTCCG
1001 GTTAACCGGA ATTGGTCCAC CGGCACCGGA TAATTTGAT TATCTTCATG
1051 AAGTTGGGTG TAAGCTGGCT CATTTAGCTG AGGCGATTCA CGTTGAGTTT
1101 GAGTACAGAG GATTTGTGGC TAACACTTTA GCTGATCTTG ATGCTTCGAT
1151 GCTTGAGCTT AGACCAAGTG AGATTGAATC TGTGCGGTT AACTCTGTTT
1201 TCGAGCTTCA CAAGCTCTTG GGACGACCTG GTGCGATCGA TAAGGTTCTT
1251 GGTGTGGTGA ATCAGATTAA ACCGGAGATT TTCACTGTGG TTGAGCAGGA
1301 ATCGAACCAT AATAGTCCGA TTTTCTTAGA TCGGTTTACT GAGTCGTTGC
1351 ATTATTACTC GACGTTGTTT GACTCGTTGG AAGGTGTACC GAGTGGTCAA
1401 GACAAGGTCA TGTCGGAGGT TTACTTGGGT AAACAGATCT GCAACGTTGT
1451 GGCTTGTGAT GGACCTGACC GAGTTGAGCG TCATGAAACG TTGAGTCAGT
1501 GGAGGAACCG GTTCGGGTCT GCTGGGTTTG CGGCTGCACA TATTGGTTCTG
1551 AATGCGTTTA AGCAAGCGAG TATGCTTTTG GCTCTGTTCA ACGGCGGTGA
1601 GGGTTATCGG GTGGAGGAGA GTGACGGCTG TCTCATGTTG GG



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Figure 6(d)

1 MKRDHHHHHQ DKKTMMNNEE DDGNGMDVAQ KLEQLEVMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSNQGGGG DTYTTNKRLK CSNGVVETTT ATAESTRHVV LVDSQENGVR
151 LVHALLACAE AVQKENLTVA EALVKQIGFL AVSQIGAMRK VATYFAEALA
201 RRIYRLSPSQ SPIDHSLSDT LQMHFYETCP YLKFAHFTAN QAILEAFQ GK
251 KRVHVIDSL*



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Figure 6(e)

1 TAGAAGTGGT AGTGGAGTGA AAAAACAAAT CCTAAGCAGT CCTAACCGAT
51 CCCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACCTCGAGC
251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA
351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
401 TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTCCG TATCGATTCTG
451 GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA
501 GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
551 AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CGGTGTGCGT
601 CTCGTTACCG CGCTTTTGGC TTGCGCTGAA GCTGTTTCTG AGGAGAATCT
651 GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTTCTC
701 AAATCGGAGC TATGAGAAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
751 CGGCGGATTT ACCGTCTCTC TCCGTGCGAG AGTCCAATCG ACCACTCTCT
801 CTCCGATACT CTTGAGATGC ACTTCTACGA GACTTGTCCT TATCTCAAGT
851 TCGCTCACTT CACGGCGAAT CAAGCGATTC TCGAAGCTTT TCAAGGGAAG
901 AAAAGAGTTC ATGTCATGTA TTTCTCTATG AGTCAAGGTC TTGGGCGCTT
951 ATGCAGGCTC TTGCGCTTCG ACCTGGTGGT CCTCCTGTTT TCCGGTTAAC
1001 CGGAATTGGT CCACCGGCAC CGGATAATTT CGATTATCTT CATGAAGTTG
1051 GGTGTAAGCT GGCTCATTTA GCTGAGGCGA TTCACGTTGA GTTTGAGTAC
1101 AGAGGATTTG TGGCTAACAC TTTAGCTGAT CTTGATGCTT CGATGCTTGA
1151 GCTTAGACCA AGTGAGATTG AATCTGTTGC GGTAACTCT GTTTTCGAGC
1201 TTCACAAGCT CTTGGGACGA CCTGGTGCGA TCGATAAGGT TCTTGGTGTG
1251 GTGAATCAGA TTAAACCGGA GATTTTCACT GTGGTTGAGC AGGAATCGAA
1301 CCATAATAGT CCGATTTTCT TAGATCGGTT TACTGAGTCG TTGCATTATT
1351 ACTCGACGTT GTTTGACTCG TTGGAAGGTG TACCGAGTGG TCAAGACAAG
1401 GTCATGTCGG AGGTTTACTT GGGTAAACAG ATCTGCAACG TTGTGGCTTG
1451 TGATGGACCT GACCGAGTTG AGCGTCATGA AACGTTGAGT CAGTGGAGGA
1501 ACCGGTTCGG GTCTGCTGGG TTTGCGGCTG CACATATTGG TTCGAATGCG
1551 TTTAAGCAAG CGAGTATGCT TTTGGCTCTG TTCAACGGCG GTGAGGGTTA
1601 TCGGGTGGAG GAGAGTGACG GCTGTCTCAT GTTGGG



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Figure 6(f)

1 MKRDHHHHHQ DKKTMMNNEE DDGNGMDVAQ KLEQLEVMMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTTNKRLK CSNGVVETTT ATAESTRHVV LVDSQENGVR
151 LVHALLACAE AVQKENLTVA EALVKQIGFL AVSQIGAMRK VATYFAEALA
201 RRIYRLSPSQ SPIDHSLSDT LQMHFYETCP YLKFAHFTAN QAILEAFQ GK
251 KRVHVIDFSM SQGLGRLCRL LRFDLVVLLF SG*



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Figure 6(g)

1 TAGAAGTGGT AGTGGAGTGA AAAAACAAAT CCTAAGCAGT CCTAACCGAT
51 CCCC GAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTGCTCAG AAACCTCGAGC
251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
301 GCTACTGAGA CTGTTCAC TAATCCGGCG GAGCTTTACA CGTGGCTTGA
351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
401 TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTCGC TATCGATTCTG
451 GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA
501 GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
551 AGTCAACTCG GCATGTGTCC TGGTTGACTC GCAGGAGAAC GGTGTGCGTC
601 TCGTTCACGC GCTTTTGGCT TCGCTGAAG CTGTTTCAGAA GGAGAATCTG
651 ACTGTGGCGG AAGCTCTGGT GAAGCAAATC GGATTCTTAG CTGTTTCTCA
701 AATCGGAGCT ATGAGAAAAG TCGCTACTTA CTTGCGCGAA GCTCTCGCGC
751 GCGGATTTA CCGTCTCTCT CCGTCGCAGA GTCCAATCGA CCACTCTCTC
801 TCCGATACTC TTCAGATGCA CTTCTACGAG ACTTGTCCTT ATCTCAAGTT
851 CGCTCACTTC ACGGCGAATC AAGCGATTCT CGAAGCTTTT CAAGGGAAGA
901 AAAGAGTTCA TGTCATTGAT TTCTCTATGA GTCAAGGTCT TCAATGGCCG
951 GCGCTTATGC AGGCTCTTGC GCTTCGACCT GGTGGTCCTC CTGTTTCCG
1001 GTTAACCGGA ATTGGTCCAC CGGCACCGGA TAATTTTCGAT TATCTTCATG
1051 AAGTTGGGTG TAAGCTGGCT CATTAGCTG AGGCGATTCA CGTTGAGTTT
1101 GAGTACAGAG GATTGTGGC TAACACTTTA GCTGATCTTG ATGCTTCGAT
1151 GCTTGAGCTT AGACCAAGTG AGATTGAATC TGTGCGGTT AACTCTGTTT
1201 TCGAGCTTCA CAAGCTCTTG GGACGACCTG GTGCGATCGA TAAGGTCTT
1251 GGTGTGGTGA ATCAGATTAA ACCGGAGATT TTCACTGTGG TTGAGCAGGA
1301 ATCGAACCAT AATAGTCCGA TTTTCTTAGA TCGGTTTACT GAGTCGTTGC
1351 ATTATTACTC GACGTTGTTT GACTCGTTGG AAGGTGTACC GAGTGGTCAA
1401 GACAAGGTCA TGTCGGAGGT TTA CTGTTGGT AAACAGATCT GCAACGTTGT
1451 GGCTTGATGAT GGACCTGACC GAGTTGAGCG TCATGAAACG TTGAGTCAGT
1501 GGAGGAACCG GTTCGGGTCT GCTGGGTTTG CGGCTGCACA TATTGGTTCG
1551 AATGCGTTTA AGCAAGCGAG TATGCTTTTG GCTCTGTTCA ACGGCGGTGA
1601 GCGTTATCGG GTGGAGGAGA GTGACGGCTG TCTCATGTTG GG



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Figure 6(h)

1 MKRDHHHHHQ DKKTTMMNEE DDGNGMDVAQ KLEQLEVTMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTTNKRLK CSNGVVETTT ATAESTRHVS WLTRRRRTVCV
151 SFTRFWLALK LFRRRI*